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Sequence Listing was accepted.

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Reviewer: markspencer

Timestamp: Mon Sep 10 13:56:07 EDT 2007

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Application No: 10598965 Version No: 3.0

Input Set:

Output Set:

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Finished: 2007-08-21 16:34:40.432  
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 435 ms  
Total Warnings: 6  
Total Errors: 0  
No. of SeqIDs Defined: 7  
Actual SeqID Count: 7

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W 213	Artificial or Unknown found in <213> in SEQ ID (5)
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# SEQUENCE LISTING

<110> Wei, Xin  
 Gariepy , Jean

<120> LIBRARY OF HETEROMERIC TOXIN MUTANTS, AND METHODS OF USING SAME

<130> 34104-0082

<140> 10598965

<141> 2007-08-21

<160> 7

<170> PatentIn version 3.2

<210> 1

<211> 299

<212> PRT

<213> Escherichia coli

<220>

<221> misc\_feature

<223> Wild type SLT-1 A chain

<400> 1

Ile	Glu	Gly	Arg	Ala	Ser	Lys	Glu	Phe	Thr	Leu	Asp	Phe	Ser	Thr	Ala
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Lys	Thr	Tyr	Val	Asp	Ser	Leu	Asn	Val	Ile	Arg	Ser	Ala	Ile	Gly	Thr
			20					25						30	

Pro	Leu	Gln	Thr	Ile	Ser	Ser	Gly	Gly	Thr	Ser	Leu	Leu	Met	Ile	Asp
		35					40						45		

Ser	Gly	Ser	Gly	Asp	Asn	Leu	Phe	Ala	Val	Asp	Val	Arg	Gly	Ile	Asp
	50					55					60				

Pro	Glu	Glu	Gly	Arg	Phe	Asn	Asn	Leu	Arg	Leu	Ile	Val	Glu	Arg	Asn
65					70					75					80

Asn	Leu	Tyr	Val	Thr	Gly	Phe	Val	Asn	Arg	Thr	Asn	Asn	Val	Phe	Tyr
			85						90					95	

Arg	Phe	Ala	Asp	Phe	Ser	His	Val	Thr	Phe	Pro	Gly	Thr	Thr	Ala	Val
			100						105					110	

Thr	Leu	Ser	Gly	Asp	Ser	Ser	Tyr	Thr	Thr	Leu	Gln	Arg	Val	Ala	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

115

120

125

Ile Ser Arg Thr Gly Met Gln Ile Asn Arg His Ser Leu Thr Thr Ser  
 130 135 140

Tyr Leu Asp Leu Met Ser His Ser Gly Thr Ser Leu Thr Gln Ser Val  
 145 150 155 160

Ala Arg Ala Met Leu Arg Phe Val Thr Val Thr Ala Glu Ala Leu Arg  
 165 170 175

Phe Arg Gln Ile Gln Arg Gly Phe Arg Thr Thr Leu Asp Asp Leu Ser  
 180 185 190

Gly Arg Ser Tyr Val Met Thr Ala Glu Asp Val Asp Leu Thr Leu Asn  
 195 200 205

Trp Gly Arg Leu Ser Ser Val Leu Pro Asp Tyr His Gly Gln Asp Ser  
 210 215 220

Val Arg Val Gly Arg Ile Ser Phe Gly Ser Ile Asn Ala Ile Leu Gly  
 225 230 235 240

Ser Val Ala Leu Ile Leu Asn Cys His His His Ala Ser Arg Val Ala  
 245 250 255

Arg Met Ala Ser Asp Glu Phe Pro Ser Met Cys Pro Ala Asp Gly Arg  
 260 265 270

Val Arg Gly Ile Thr His Asn Lys Ile Leu Trp Asp Ser Ser Thr Leu  
 275 280 285

Gly Ala Ile Leu Met Arg Arg Thr Ile Ser Ser  
 290 295

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<212> DNA

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gttactgtga cagctgaagc ttacgtttt cg

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31

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<211> 302  
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<213> Artificial

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1 5 10 15

Arg Ala Ser Lys Glu Phe Thr Leu Asp Phe Ser Thr Ala Lys Thr Tyr  
20 25 30

Val Asp Ser Leu Asn Val Ile Arg Ser Ala Ile Gly Thr Pro Leu Gln  
35 40 45

Thr Ile Ser Ser Gly Gly Thr Ser Leu Leu Met Ile Asp Ser Gly Ser  
50 55 60

Gly Asp Asn Leu Phe Ala Val Asp Val Arg Gly Ile Asp Pro Glu Glu  
65 70 75 80

Gly Arg Phe Asn Asn Leu Arg Leu Ile Val Glu Arg Asn Asn Leu Tyr  
85 90 95

Val Thr Gly Phe Val Asn Arg Thr Asn Asn Val Phe Tyr Arg Phe Ala  
100 105 110

Asp Phe Ser His Val Thr Phe Pro Gly Thr Thr Ala Val Thr Leu Ser  
115 120 125

Gly Asp Ser Ser Tyr Thr Thr Leu Gln Arg Val Ala Gly Ile Ser Arg

130

135

140

Thr Gly Met Gln Ile Asn Arg His Ser Leu Thr Thr Ser Tyr Leu Asp  
 145 150 155 160

Leu Met Ser His Ser Gly Thr Ser Leu Thr Gln Ser Val Ala Arg Ala  
 165 170 175

Met Leu Arg Phe Val Thr Val Thr Ala Glu Ala Leu Arg Phe Arg Gln  
 180 185 190

Ile Gln Arg Gly Phe Arg Thr Thr Leu Asp Asp Leu Ser Gly Arg Ser  
 195 200 205

Tyr Val Met Thr Ala Glu Asp Val Asp Leu Thr Leu Asn Trp Gly Arg  
 210 215 220

Leu Ser Ser Val Leu Pro Asp Tyr His Gly Gln Asp Ser Val Arg Val  
 225 230 235 240

Gly Arg Ile Ser Phe Gly Ser Ile Asn Ala Ile Leu Gly Ser Val Ala  
 245 250 255

Leu Ile Leu Asn Cys His His His Ile Tyr Ser Asn Lys Leu Met Ala  
 260 265 270

Ser Arg Val Ala Arg Met Ala Ser Asp Glu Phe Pro Ser Met Cys Pro  
 275 280 285

Ala Asp Gly Arg Val Arg Gly Ile Thr His Asn Lys Ile Leu  
 290 295 300

&lt;210&gt; 5

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; SLT-1 A Chain lib#5 protein sequence (SAM5)

&lt;400&gt; 5

Lys Gly Met Arg Ser His His His His His His His His Ile Glu Gly  
 1 5 10 15

Arg Ala Ser Lys Glu Phe Thr Leu Asp Phe Ser Thr Ala Lys Thr Tyr  
20 25 30

Val Asp Ser Leu Asn Val Ile Arg Ser Ala Ile Gly Thr Pro Leu Gln  
35 40 45

Thr Ile Ser Ser Gly Gly Thr Ser Leu Leu Met Ile Asp Ser Gly Ser  
50 55 60

Gly Asp Asn Leu Phe Ala Val Asp Val Arg Gly Ile Asp Pro Glu Glu  
65 70 75 80

Gly Arg Phe Asn Asn Leu Arg Leu Ile Val Glu Arg Asn Asn Leu Tyr  
85 90 95

Val Thr Gly Phe Val Asn Arg Thr Asn Asn Val Phe Tyr Arg Phe Ala  
100 105 110

Asp Phe Ser His Val Thr Phe Pro Gly Thr Thr Ala Val Thr Leu Ser  
115 120 125

Gly Asp Ser Ser Tyr Thr Thr Leu Gln Arg Val Ala Gly Ile Ser Arg  
130 135 140

Thr Gly Met Gln Ile Asn Arg His Ser Leu Thr Thr Ser Tyr Leu Asp  
145 150 155 160

Leu Met Ser His Ser Gly Thr Ser Leu Thr Gln Ser Val Ala Arg Ala  
165 170 175

Met Leu Arg Phe Val Thr Val Thr Ala Glu Ala Leu Arg Phe Arg Gln  
180 185 190

Ile Gln Arg Gly Phe Arg Thr Thr Leu Asp Asp Leu Ser Gly Arg Ser  
195 200 205

Tyr Val Met Thr Ala Glu Asp Val Asp Leu Thr Leu Asn Trp Gly Arg  
210 215 220

Leu Ser Ser Val Leu Pro Asp Tyr His Gly Gln Asp Ser Val Arg Val  
225 230 235 240

Gly Arg Ile Ser Phe Gly Ser Ile Asn Ala Ile Leu Gly Ser Val Ala

245

250

255

Leu Ile Leu Asn Cys His His His Ala Ala Phe Ala Asp Leu Ile Ala  
260 265 270

Ser Arg Val Ala Arg Met Ala Ser Asp Glu Phe Pro Ser Met Cys Pro  
275 280 285

Ala Asp Gly Arg Val Arg Gly Ile Thr His Asn Lys Ile Leu Trp Asp  
290 295 300

Ser Ser Thr Leu Gly Ala Ile Leu Met Arg Arg Thr Ile Ser Ser  
305 310 315

&lt;210&gt; 6

&lt;211&gt; 7

&lt;212&gt; PRT

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; First melanoma active insert

&lt;400&gt; 6

Ile Tyr Ser Asn Lys Leu Met  
1 5

&lt;210&gt; 7

&lt;211&gt; 7

&lt;212&gt; PRT

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; Second melanoma active insert

&lt;400&gt; 7

Ala Ala Phe Ala Asp Leu Ile  
1 5